



FY

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/673,994  
Source: PG/09  
Date Processed by STIC: 2/13/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/673,994

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,994

DATE: 02/13/2002

TIME: 07:45:38

Input Set : A:\B08017197.txt

Output Set: N:\CRF3\02132002\I673994.raw

Does Not Comply  
Corrected Diskette Needed

ppr 1-2, 4-6

3 <110> APPLICANT: Chen, Yuqing E.  
 4 Tamura, Koichi  
 5 Horiuchi, Masatsugu  
 6 Dzau, Victor J.  
 8 <120> TITLE OF INVENTION: CNRE Binding Factors and Uses Thereof  
 10 <130> FILE REFERENCE: B0801/7197/ERG/KA  
 12 <140> CURRENT APPLICATION NUMBER: US 09/673994  
 13 <141> CURRENT FILING DATE: 2000-10-24  
 15 <150> PRIOR APPLICATION NUMBER: US 60/082,997  
 16 <151> PRIOR FILING DATE: 1998-04-24  
 18 <150> PRIOR APPLICATION NUMBER: PCT/US99/08502  
 19 <151> PRIOR FILING DATE: 1999-04-23  
 21 <160> NUMBER OF SEQ ID NOS: 23  
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0

## ERRORED SEQUENCES

307 <210> SEQ ID NO: 7  
 308 <211> LENGTH: 3847  
 309 <212> TYPE: DNA  
 310 <213> ORGANISM: Mus musculus  
 312 <400> SEQUENCE: 7

ppr 1-2

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E--> 314	<u>gttattgtca tccattgtgg aagaggtgag tctaaagttg ggagggaggn gnttggnta</u>	120	> see
E--> 315	<u>aaacaganaa ttttttttga gatgtgagca gaggttgga gttagattca ctgaanacaa</u>	180	
E--> 316	<u>ttagtgactt tgattaaaan gngggttntt tcttcatttc ccagatgtag cctgggcttc</u>	240	> item 9
E--> 317	<u>agaaattnac ngtttttttt tttgtgataa cttgcccatt ctttgtgtcc tgctttcttg</u>	300	on Enov
318	tatttagcaag gacaagcttt cttgtgtgtac tttggttcaa accccatggc taaactgcct	360	Summary
319	taaccttttt gtagctgctg gatcagtgcc tggcgccaga cacttctggg gatggtacag	420	Sheet
320	ggtgtgacaa catgacgtgc atcatcattt gtttcaagcc ccgaaacaca gtagagcttc	480	
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324	agcagtgggg atgaggtgtg cagggggctg ggtggctttc ctcagcccat tacaagagg	720	
325	gccccccacc cccccacgc ggcagcctgg gaggtctgct tgtcctctta agcctcctta	780	
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327	gactggtagt tctgattttt actctgtgaa cactttattt aaggacattc ttttttattg	900	
328	gcggctctgt gacccttagc cgcttgaccc cgctctctgt tgtacacttt caagcaacac	960	
329	tttttcagac taaaggccaa acaaaagcta atcgtgctca tagtgtcatg ctttactctc	1020	
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331	tctggagagg gggcagtgaa tgtggagcag gagctgggag tcttaactcc tgagtaagca	1140	
332	gcccgtgga ggccatcctg cgctgttcgc cttcaggcac gacttcctag ttcgtatatg	1200	

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Input Set : A:\B08017197.txt

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 334 ggttggttag cagcgcatca caatcacttc ctggtcatgc tgcgactgcg ctccggttgt 1320  
 335 acagcccatg aactacgcat cccgtgttgc tctgcggtgg cggaagcgga agcgggtacg 1380  
 336 gaggtaccag ctggtcttcg gaggggggta gggggctcca tgaatggaag cggcggcggc 1440  
 337 ggcgggagcg acctgagctg gattccgggg ccggggcagg ggctgcccag ggccgcacc 1500  
 338 gtgtatggg gcggttcgtg gatcctaaga gcaaggaccg acggcagggc cgaactggga 1560  
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 341 aggggccttg agccgggagg aacaggggtg gggtcagtag agtgggctca ggtcaggggtg 1740  
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 343 ttaaaggaaac ctgaggggtca tcgagtacgg gaagtgcagt tcacaacagc tggctccttg 1860  
 344 gttcggatta tgggtactgc ttgggagggg gattccacaa gcacctccc ctctttagt 1920  
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 346 ctaggccaag atctggagtt tgaagaggaa gaggaagagg atgaaggtga cggccacaac 2040  
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 348 cttccctatg ggctgagtga cgacgagtct gggggcgggc gcgcaactaag tgcggagagt 2160  
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 E--> 353 **tgaggccgct gcccatacgc ntcagccag ttcgtcaacc tgacgcgaca taccgcacc** 2460 *Item 9*  
 354 cactactggcg agaagcccta ccgttgctcc cactgcccct ttgcctgcag cagcctgggc 2520  
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 366 ggtgacaaac cttttcggtg tagcctttgc aactacagct gcaaccagag tatgaacctc 3240  
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 379 <210> SEQ ID NO: 8  
 380 <211> LENGTH: 763  
 381 <212> TYPE: PRT  
 382 <213> ORGANISM: Mus musculus

## RAW SEQUENCE LISTING

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Input Set : A:\B08017197.txt

Output Set: N:\CRF3\02132002\I673994.raw

384 &lt;400&gt; SEQUENCE: 8

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385 Met Glu Gly Ala Gly Tyr His Leu Pro Gly Trp Leu Val Gly Leu Arg
386 1 5 10 15
387 Val Gln Leu Leu Ile Gly Trp Leu Ala Ala His His Asn His Phe Leu
388 20 25 30
389 Val Met Leu Arg Leu Arg Ser Gly Cys Thr Ala His Glu Leu Arg Ile
390 35 40 45
391 Pro Cys Cys Ser Ala Val Ala Glu Ala Glu Ala Gly Thr Glu Val Pro
392 50 55 60
393 Ala Gly Leu Arg Arg Gly Val Gly Gly Ser Met Asn Gly Ser Gly Gly
394 65 70 75 80
395 Gly Gly Gly Ser Asp Leu Ser Trp Ile Pro Gly Pro Gly Gln Gly Leu
396 85 90 95
397 Pro Arg Ala Arg Thr Val Tyr Gly Gly Gly Ser Trp Ile Leu Arg Ala
398 100 105 110
399 Arg Thr Asp Gly Arg Ala Glu Leu Gly Gly Ala Gly Pro Gly Gly Leu
400 115 120 125
401 Gly Pro Glu Ala Arg Arg Ala Gly Ala Gly His Asp Ala Pro Lys Glu
402 130 135 140
403 Ala Lys Pro Ser Thr Ala Arg Glu Met Arg Gly Gly Gln Arg Ser Gly
404 145 150 155 160
405 Val Arg Gly Leu Glu Pro Gly Gly Thr Gly Val Gly Ser Val Glu Trp
406 165 170 175
407 Ala Gln Val Arg Val Glu Gly Asp Ser Ser Gly Leu Gly Ala Asp Asp
408 180 185 190
409 Leu Gly Ser Ser Leu Leu Thr Arg Val Leu Lys Glu Pro Glu Gly His
410 195 200 205
411 Arg Val Arg Glu Val Gln Phe Thr Thr Ala Gly Ser Leu Val Arg Ile
412 210 215 220
413 Met Gly Thr Ala Trp Glu Gly Asp Ser Thr Ser Thr Leu Pro Ser Leu
414 225 230 235 240
415 Val Asp Thr Glu Asp Ser Phe Asp Glu Gly Pro Gly Ala Leu Val Leu
416 245 250 255
417 Glu Ser Asp Leu Leu Leu Gly Gln Asp Leu Glu Phe Glu Glu Glu
418 260 265 270
419 Glu Glu Asp Glu Gly Asp Gly His Asn Asp Gln Leu Met Gly Phe Glu
420 275 280 285
421 Arg Asp Ser Glu Gly Asp Ser Gln Gly Ala Arg Pro Gly Leu Pro Tyr
422 290 295 300
423 Gly Leu Ser Asp Asp Glu Ser Gly Gly Gly Arg Ala Leu Ser Ala Glu
424 305 310 315 320
425 Ser Glu Val Glu Glu Pro Ala Arg Gly Pro Gly Glu Ala Arg Gly Glu
426 325 330 335
427 Arg Pro Gly Pro Ala Cys Gln Leu Cys Gly Gly Pro Thr Gly Glu Gly
428 340 345 350
429 Pro Cys Cys Gly Ala Gly Gly Arg Gly Gly Gly Pro Pro Leu Pro Pro
430 355 360 365
431 Arg Leu Leu Tyr Ser Cys Arg Leu Cys Ala Phe Val Ser His Tyr Ser
432 370 375 380

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Input Set : A:\B08017197.txt

Output Set: N:\CRF3\02132002\I673994.raw

433 Ser His Leu Lys Arg His Met Gln Thr His Ser Gly Glu Lys Pro Phe  
 434 385 390 395 400  
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 436 405 410 415  
 437 Arg His Thr Arg Thr His Thr Gly Glu Lys Pro Tyr Arg Cys Pro His  
 438 420 425 430  
 439 Cys Pro Phe Ala Cys Ser Ser Leu Gly Asn Leu Arg Arg His Gln Arg  
 440 435 440 445  
 441 Thr His Thr Gly Pro Pro Thr Pro Pro Cys Pro Thr Cys Gly Phe Arg  
 442 450 455 460  
 443 Cys Cys Ala Pro Arg Pro Thr Arg Pro Pro Ser Pro Thr Glu Gln Glu  
 444 465 470 475 480  
 445 Gly Thr Met Pro Arg Arg Ser Glu Asn Ala Leu Ile Leu Pro Asp Leu  
 446 485 490 495  
 447 Ser Leu His Val Pro Pro Gly Gly Ala Ser Phe Leu Pro Asp Cys Gly  
 448 500 505 510  
 449 Gln Leu Arg Gly Glu Gly Glu Ser Leu Cys Gly Thr Gly Ser Glu Pro  
 450 515 520 525  
 451 Leu Pro Glu Leu Leu Phe Pro Trp Thr Cys Arg Gly Cys Gly Gln Glu  
 452 530 535 540  
 453 Leu Glu Glu Gly Glu Gly Ser Arg Leu Gly Ala Ala Met Cys Gly Arg  
 454 545 550 555 560  
 455 Cys Met Arg Gly Glu Ala Gly Gly Val Ala Thr Gly Gly Pro Gln Gly  
 456 565 570 575  
 457 Pro Gly Asp Lys Gly Phe Ala Cys Ser Leu Cys Pro Phe Ala Thr His  
 458 580 585 590  
 459 Tyr Pro Asn His Leu Ala Arg His Met Lys Thr His Ser Gly Glu Lys  
 460 595 600 605  
 461 Pro Phe Arg Cys Ala Arg Cys Pro Tyr Ala Ser Ala His Leu Asp Asn  
 462 610 615 620  
 463 Leu Lys Arg His Gln Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys  
 464 625 630 635 640  
 465 Pro Leu Cys Pro Tyr Ala Cys Gly Asn Leu Ala Asn Leu Lys Arg His  
 466 645 650 655  
 467 Gly Arg Ile His Ser Gly Asp Lys Pro Phe Arg Cys Ser Leu Cys Asn  
 468 660 665 670  
 469 Tyr Ser Cys Asn Gln Ser Met Asn Leu Lys Arg His Met Leu Arg His  
 470 675 680 685  
 471 Thr Gly Glu Lys Pro Phe Arg Cys Ala Thr Cys Ala Tyr Thr Thr Gly  
 472 690 695 700  
 473 His Trp Asp Asn Tyr Lys Arg His Gln Lys Val His Gly His Gly Gly  
 474 705 710 715 720  
 475 Ala Gly Gly Pro Gly Leu Ser Ala Pro Glu Gly Trp Ala Pro Pro His  
 476 725 730 735  
 477 Ser Pro Pro Ser Val Leu Ser Thr Arg Gly Pro Ala Ala Leu Gly Ala  
 478 740 745 750  
 479 Thr Gly Ser Arg Ala Leu His Ser Asp Ser Pro  
 480 755 760  
 482 <210> SEQ ID NO: 9

*see*  
*Item 9*

## RAW SEQUENCE LISTING

DATE: 02/13/2002

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TIME: 07:45:38

Input Set : A:\B08017197.txt

Output Set: N:\CRF3\02132002\I673994.raw

483 &lt;211&gt; LENGTH: 2289

484 &lt;212&gt; TYPE: DNA

485 &lt;213&gt; ORGANISM: Mus musculus

487 &lt;400&gt; SEQUENCE: 9

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 490 tgtacagccc atgaactacg catcccgtgt tgctctgcgg tggcggaagc ggaagcgggt 180  
 491 acggaggtac cagctggtct tcggaggggg gttagggggt ccatgaatgg aagcggcggc 240  
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 493 accgtgtatg ggggcggttc gtggatccta agagcaagga ccgacggcag ggccgaactg 360  
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 498 gtattaaagg aacctgaggg tcatcgagta cgggaagtgc agttcacaac agctggctcc 660  
 499 ttggttcgga ttatgggtac tgcttgggag ggagattcca caagcaccct cccctcttta 720  
 500 gtggatactg aagattcctt cgacgaaggc cctggggccc tgggtgttga gagcgatttg 780  
 501 ctactaggcc aagatctgga gtttgaagag gaagaggaag aggatgaagg tgacggccac 840  
 502 aacgaccagc tcatgggctt tgagagagac tctgaaggag actctcaggg ggccagacct 900  
 503 ggacttcctt atgggctgag tgacgacgag tctgggggag gccgcgcact aagtgcggag 960  
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 507 tcccactact cgagccacct gaagcggcac atgcagacac acagcgggga gaagcgttc 1200  
 E--> 508 cgctgtggcc gctgcccata cgctcagcc cagttcgtca acctgacgag acataccgcg 1260 *Item 9*  
 509 acccatactg gcgagaagcc ctaccgttgt cccactgcc cctttgcctg cagcagcctg 1320  
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 523 tataccacag gccactggga caactacaag cgtcatcaga aggtgcatgg ccatggtgga 2160  
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 607 <211> LENGTH: 581  
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 609 <213> ORGANISM: Mus musculus *P. 6*  
 611 <400> SEQUENCE: 15  
 612 ggccttttagt ctgaaaaagt gttgcttgaa agtggtacaac agagagcggg tgcaagcggc 60

## RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/09/673,994

TIME: 07:45:38

Input Set : A:\B08017197.txt

Output Set: N:\CRF3\02132002\I673994.raw

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614 aaatcagaac taccagtcct tccctccaac acaacagagc acaggcacag aaccgatagt 180
615 cgatgagccc aaggagagta aggaggctta agaggacagc agagcctccc aggctgccgc 240
616 gtgggggggg tgggggggccc tctttgtaat gggctgagga aagccacca gcccctgca 300
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624 <211> LENGTH: 586
625 <212> TYPE: DNA
626 <213> ORGANISM: Mus musculus
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item 9

item 9



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/673,994

DATE: 02/13/2002

TIME: 07:45:39

Input Set : A:\B08017197.txt

Output Set: N:\CRF3\02132002\I673994.raw

L:314 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7

M:340 Repeated in SeqNo=7

L:435 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8

L:508 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9

L:620 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15

L:637 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16